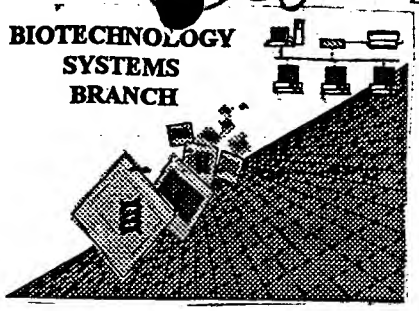
OIPE JC169
JUN 28 2001
PATENT & TRADEMARK OFFICE

T3 6300 0889

RAW SEQUENCE LISTING ERROR REPORT



RECEIVED
JUL 03 2001
TECH CENTER 1600/2900

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/724,126

Source: OIPE

Date Processed by STIC: 12/7/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

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Raw Sequence Listing Error Summary

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ERROR DETECTED	SUGGESTED CORRECTION

SERIAL NUMBER: 09/724,126

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

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OIPE

RAW SEQUENCE LISTING DATE: 12/07/2000
PATENT APPLICATION: US/09/724,126 TIME: 07:57:43

Input Set : A:\35966aseq.txt
Output Set: N:\CRF3\12072000\I724126.raw

Does Not Comply
Corrected Diskette Needed

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  4 <110> APPLICANT: Han, Hui-Quan
  5       Kwak, Keith
  7 <120> TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase
  9 <130> FILE REFERENCE: 01017/35966
OK> 11 <140> CURRENT APPLICATION NUMBER: US/09/724,126
OK> 12 <141> CURRENT FILING DATE: 2000-11-28
 14 <150> PRIOR APPLICATION NUMBER: US 60/187,911
 15 <151> PRIOR FILING DATE: 1999-03-08
 17 <160> NUMBER OF SEQ ID NOS: 29
 19 <170> SOFTWARE: PatentIn Ver. 2.0
```

ERRORED SEQUENCES

pg 45

```
508 <210> SEQ ID NO: 2
509 <211> LENGTH: 1749
510 <212> TYPE: PRT
511 <213> ORGANISM: Homo sapiens
513 <400> SEQUENCE: 2
514 Met Ala Asp Glu Glu Ala Gly Gly Thr Glu Arg Met Glu Ile Ser Ala
515   1               5                  10                  15
517 Glu Leu Pro Gln Thr Pro Gln Arg Leu Ala Ser Trp Trp Asp Gln Gln
518               20                  25                  30
520 Val Asp Phe Tyr Thr Ala Phe Leu His His Leu Ala Glu Leu Val Pro
521           35                  40                  45
523 Glu Ile Tyr Phe Ala Glu Met Asp Pro Asp Leu Glu Lys Gln Glu Glu
524       50                  55                  60
526 Ser Val Gln Met Ser Ile Phe Thr Pro Leu Glu Trp Tyr Leu Phe Gly
527   65                  70                  75                  80
529 Glu Asp Pro Asp Ile Cys Leu Glu Lys Leu Lys His Ser Gly Ala Phe
530                   85                  90                  95
532 Gln Leu Cys Gly Arg Val Phe Lys Ser Gly Glu Thr Thr Tyr Ser Cys
533               100                 105                 110
535 Arg Asp Cys Ala Ile Asp Pro Thr Cys Val Leu Cys Met Asp Cys Phe
536           115                 120                 125
538 Gln Asp Ser Val His Lys Asn His Arg Tyr Lys Met His Thr Ser Thr
539       130                 135                 140
541 Gly Gly Gly Phe Cys Asp Cys Gly Asp Thr Glu Ala Trp Lys Thr Gly
542 145                 150                 155                 160
544 Pro Phe Cys Val Asn His Glu Pro Gly Arg Ala Gly Thr Ile Lys Glu
545                 165                 170                 175
547 Asn Ser Arg Cys Pro Leu Asn Glu Glu Val Ile Val Gln Ala Arg Lys
548             180                 185                 190
550 Ile Phe Pro Ser Val Ile Lys Tyr Val Val Glu Met Thr Ile Trp Glu
551         195                 200                 205
553 Glu Glu Lys Glu Leu Pro Pro Glu Leu Gln Ile Arg Glu Lys Asn Glu
554     210                 215                 220
```

RAW SEQUENCE LISTING DATE: 12/07/2000
PATENT APPLICATION: US/09/724,126 TIME: 07:57:43

Input Set : A:\35966aseq.txt
Output Set: N:\CRF3\12072000\I724126.raw

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556 Arg Tyr Tyr Cys Val Leu Phe Asn Asp Glu His His Ser Tyr Asp His
557 225                 230                 235                 240
559 Val Ile Tyr Ser Leu Gln Arg Ala Leu Asp Cys Glu Leu Ala Glu Ala
560                 245                 250                 255
562 Gln Leu His Thr Thr Ala Ile Asp Lys Glu Gly Arg Arg Ala Val Lys
563             260                 265                 270
565 Ala Gly Ala Tyr Ala Ala Cys Gln Glu Ala Lys Glu Asp Ile Lys Ser
566         275                 280                 285
568 His Ser Glu Asn Val Ser Gln His Pro Leu His Val Glu Val Leu His
569     290                 295                 300
571 Ser Glu Ile Met Ala His Gln Lys Phe Ala Leu Arg Leu Gly Ser Trp
572 305                 310                 315                 320
574 Met Asn Lys Ile Met Ser Tyr Ser Ser Asp Phe Arg Gln Ile Phe Cys
575                 325                 330                 335
577 Gln Ala Cys Leu Arg Glu Glu Pro Asp Ser Glu Asn Pro Cys Leu Ile
578             340                 345                 350
580 Ser Arg Leu Met Leu Trp Asp Ala Lys Leu Tyr Lys Gly Ala Arg Lys
581         355                 360                 365
583 Ile Leu His Glu Leu Ile Phe Ser Ser Phe Phe Met Glu Met Glu Tyr
584     370                 375                 380
586 Lys Lys Leu Phe Ala Met Glu Phe Val Lys Tyr Tyr Lys Glu Leu Gln
587 385                 390                 395                 400
589 Lys Glu Tyr Ile Ser Asp Asp His Asp Arg Ser Ile Ser Ile Thr Ala
590                 405                 410                 415
592 Leu Ser Val Gln Met Phe Thr Val Pro Thr Leu Ala Arg His Leu Ile
593             420                 425                 430
595 Glu Glu Gln Asn Val Ile Ser Val Ile Thr Glu Thr Leu Leu Glu Val
596         435                 440                 445
598 Leu Pro Glu Tyr Leu Asp Arg Asn Asn Lys Phe Asn Phe Gln Gly Tyr
599     450                 455                 460
601 Ser Gln Asp Lys Leu Gly Arg Val Tyr Ala Val Ile Cys Asp Leu Lys
602 465                 470                 475                 480
604 Tyr Ile Leu Ile Ser Lys Pro Thr Ile Trp Thr Glu Arg Leu Arg Met
605                 485                 490                 495
607 Gln Phe Leu Glu Gly Phe Arg Ser Phe Leu Lys Ile Leu Thr Cys Met
608             500                 505                 510
610 Glu Gly Met Glu Glu Ile Arg Arg Gln Val Gly Gln His Ile Glu Val
611         515                 520                 525
613 Asp Pro Asp Trp Glu Ala Ala Ile Ala Ile Gln Met Gln Leu Lys Asn
614     530                 535                 540
616 Ile Leu Leu Met Phe Gln Glu Trp Cys Ala Cys Asp Glu Glu Leu Leu
617 545                 550                 555                 560
619 Leu Val Ala Tyr Lys Glu Cys His Lys Ala Val Met Arg Cys Ser Thr
620                 565                 570                 575
622 Ser Phe Ile Ser Ser Ser Lys Thr Val Val Gln Ser Cys Gly His Ser
623             580                 585                 590
625 Leu Glu Thr Lys Ser Tyr Arg Val Ser Glu Asp Leu Val Ser Ile His
626         595                 600                 605
628 Leu Pro Leu Ser Arg Thr Leu Ala Gly Leu His Val Arg Leu Ser Arg
```

RAW SEQUENCE LISTING DATE: 12/07/2000
PATENT APPLICATION: US/09/724,126 TIME: 07:57:43

Input Set : A:\35966aseq.txt
Output Set: N:\CRF3\12072000\I724126.raw

```
629      610                 615                 620
631 Leu Gly Ala Val Ser Arg Leu His Glu Phe Val Ser Phe Glu Asp Phe
632 625                 630                 635                 640
634 Gln Val Glu Val Leu Val Glu Tyr Pro Leu Arg Cys Leu Val Leu Val
635                 645                 650                 655
637 Ala Gln Val Val Ala Glu Met Trp Arg Arg Asn Gly Leu Ser Leu Ile
638                 660                 665                 670
640 Ser Gln Val Phe Tyr Tyr Gln Asp Val Lys Cys Arg Glu Glu Met Tyr
641         675                 680                 685
643 Asp Lys Asp Ile Ile Met Leu Gln Ile Gly Ala Ser Leu Met Asp Pro
644     690                 695                 700
646 Asn Lys Phe Leu Leu Leu Val Leu Glu Arg Tyr Glu Leu Ala Glu Ala
647 705                 710                 715                 720
649 Phe Asn Lys Thr Ile Ser Thr Lys Asp Gln Asp Leu Ile Lys Gln Tyr
650                 725                 730                 735
652 Asn Thr Leu Ile Glu Glu Met Leu Gln Val Leu Ile Tyr Ile Val Gly
653                 740                 745                 750
655 Glu Arg Tyr Val Pro Gly Val Gly Asn Val Thr Lys Glu Glu Val Thr
656         755                 760                 765
658 Met Arg Glu Ile Ile His Leu Leu Cys Ile Glu Pro Met Pro His Ser
659     770                 775                 780
661 Ala Ile Ala Lys Asn Leu Pro Glu Asn Glu Asn Asn Glu Thr Gly Leu
662 785                 790                 795                 800
664 Glu Asn Val Ile Asn Lys Val Ala Thr Phe Lys Lys Pro Gly Val Ser
665                 805                 810                 815
667 Gly His Gly Val Tyr Glu Leu Lys Asp Glu Ser Leu Lys Asp Phe Asn
668                 820                 825                 830
670 Met Tyr Phe Tyr His Tyr Ser Lys Thr Gln His Ser Lys Ala Glu His
671         835                 840                 845
673 Met Gln Lys Lys Arg Arg Lys Gln Glu Asn Lys Asp Glu Ala Leu Pro
674     850                 855                 860
676 Pro Pro Pro Pro Pro Glu Phe Cys Pro Ala Phe Ser Lys Val Ile Asn
677 865                 870                 875                 880
679 Leu Leu Asn Cys Asp Ile Met Met Tyr Ile Leu Arg Thr Val Phe Glu
680                 885                 890                 895
682 Arg Ala Ile Asp Thr Asp Ser Asn Leu Trp Thr Glu Gly Met Leu Gln
683                 900                 905                 910
685 Met Ala Phe His Ile Leu Ala Leu Gly Leu Leu Glu Glu Lys Gln Gln
686         915                 920                 925
688 Leu Gln Lys Ala Pro Glu Glu Glu Val Thr Phe Asp Phe Tyr His Lys
689     930                 935                 940
691 Ala Ser Arg Leu Gly Ser Ser Ala Met Asn Ile Gln Met Leu Leu Glu
692 945                 950                 955                 960
694 Lys Leu Lys Gly Ile Pro Gln Leu Glu Gly Gln Lys Asp Met Ile Thr
695                 965                 970                 975
697 Trp Ile Leu Gln Met Phe Asp Thr Val Lys Arg Leu Arg Glu Lys Ser
698                 980                 985                 990
700 Cys Leu Ile Val Ala Thr Thr Ser Gly Ser Glu Ser Ile Lys Asn Asp
701         995                1000                1005
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